



SEQUENCE LISTING

<110> KATO, MASARU
MIURA, YUTAKA
KETTOKU, MASAKO
IWAMATSU, AKIHIRO
KOBAYASHI, KAZUO
KOMEDA, TOSHIHIRO

<120> NOVEL TRANSFERASE AND AMYLASE, PROCESS FOR PRODUCING
THE ENZYMES, USE THEREOF, AND GENE CODING FOR THE SAME

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ttcttacgga cattcaggct gggtttacagt atactgtaga atatgtaata ggaaaaataag	3085
aataggaacg gacttagtct acaaatgccc taaatgtgaa aagaagtata acgcattctt	3145
ctgtgaagca gatgctaggg gattaaagaa aaagtgccca tactgtggta ctgaacttgt	3205

cagtgcatt taagactcaa atagaaggta aaaatatttt tatactgaat aatgagttgt 3265
 tttagcgtga tacggatata gttattcgaa atcaagattt tattaagaaa ctcaccttta 3325
 cacaatataa taagattgcc tatattgaca tggacataga aacgacagaa ttttaagatat 3385
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 <212> PRT
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 20 25 30
 Glu Thr Ala His Thr Ile Gly Leu Gly Ile Ile Gln Asp Ile Val Pro
 35 40 45
 Asn His Met Ala Val Asn Ser Leu Asn Trp Arg Leu Met Asp Val Leu
 50 55 60
 Lys Met Gly Lys Lys Ser Lys Tyr Tyr Thr Tyr Phe Asp Phe Phe Pro
 65 70 75 80
 Glu Asp Asp Lys Ile Arg Leu Pro Ile Leu Gly Glu Asp Leu Asp Thr
 85 90 95
 Val Ile Ser Lys Gly Leu Leu Lys Ile Val Lys Asp Gly Asp Glu Tyr
 100 105 110
 Phe Leu Glu Tyr Phe Lys Trp Lys Leu Pro Leu Thr Glu Val Gly Asn
 115 120 125
 Asp Ile Tyr Asp Thr Leu Gln Lys Gln Asn Tyr Thr Leu Met Ser Trp
 130 135 140
 Lys Asn Pro Pro Ser Tyr Arg Arg Phe Phe Asp Val Asn Thr Leu Ile
 145 150 155 160
 Gly Val Asn Val Glu Lys Asp His Val Phe Gln Glu Ser His Ser Lys
 165 170 175
 Ile Leu Asp Leu Asp Val Asp Gly Tyr Arg Ile Asp His Ile Asp Gly
 180 185 190
 Leu Tyr Asp Pro Glu Lys Tyr Ile Asn Asp Leu Arg Ser Ile Ile Lys
 195 200 205
 Asn Lys Ile Ile Ile Val Glu Lys Ile Leu Gly Phe Gln Glu Glu Leu
 210 215 220

Lys Leu Asn Ser Asp Gly Thr Thr Gly Tyr Asp Phe Leu Asn Tyr Ser
 225 230 235 240
 Asn Leu Leu Phe Asn Phe Asn Gln Glu Ile Met Asp Ser Ile Tyr Glu
 245 250 255
 Asn Phe Thr Ala Glu Lys Ile Ser Ile Ser Glu Ser Ile Lys Lys Ile
 260 265 270
 Lys Ala Gln Ile Ile Asp Glu Leu Phe Ser Tyr Glu Val Lys Arg Leu
 275 280 285
 Ala Ser Gln Leu Gly Ile Ser Tyr Asp Ile Leu Arg Asp Tyr Leu Ser
 290 295 300
 Cys Ile Asp Val Tyr Arg Thr Tyr Ala Asn Gln Ile Val Lys Glu Cys
 305 310 315 320
 Asp Lys Thr Asn Glu Ile Glu Glu Ala Thr Lys Arg Asn Pro Glu Ala
 325 330 335
 Tyr Thr Lys Leu Gln Gln Tyr Met Pro Ala Val Tyr Ala Lys Ala Tyr
 340 345 350
 Glu Asp Thr Phe Leu Phe Arg Tyr Asn Arg Leu Ile Ser Ile Asn Glu
 355 360 365
 Val Gly Ser Asp Leu Arg Tyr Tyr Lys Ile Ser Pro Asp Gln Phe His
 370 375 380
 Val Phe Asn Gln Lys Arg Arg Gly Lys Ile Thr Leu Asn Ala Thr Ser
 385 390 395 400
 Thr His Asp Thr Lys Phe Ser Glu Asp Val Arg Met Lys Ile Ser Val
 405 410 415
 Leu Ser Glu Phe Pro Glu Glu Trp Lys Asn Lys Val Glu Glu Trp His
 420 425 430
 Ser Ile Ile Asn Pro Lys Val Ser Arg Asn Asp Glu Tyr Arg Tyr Tyr
 435 440 445
 Gln Val Leu Val Gly Ser Phe Tyr Glu Gly Phe Ser Asn Asp Phe Lys
 450 455 460
 Glu Arg Ile Lys Gln His Met Ile Lys Ser Val Arg Glu Ala Lys Ile
 465 470 475 480
 Asn Thr Ser Trp Arg Asn Gln Asn Lys Glu Tyr Glu Asn Arg Val Met
 485 490 495
 Glu Leu Val Glu Glu Thr Phe Thr Asn Lys Asp Phe Ile Lys Ser Phe
 500 505 510
 Met Lys Phe Glu Ser Lys Ile Arg Arg Ile Gly Met Ile Lys Ser Leu
 515 520 525

Ser Leu Val Ala Leu Lys Ile Met Ser Ala Gly Ile Pro Asp Phe Tyr
 530 535 540
 Gln Gly Thr Glu Ile Trp Arg Tyr Leu Leu Thr Asp Pro Asp Asn Arg
 545 550 555 560
 Val Pro Val Asp Phe Lys Lys Leu His Glu Ile Leu Glu Lys Ser Lys
 565 570 575
 Lys Phe Glu Lys Asn Met Leu Glu Ser Met Asp Asp Gly Arg Ile Lys
 580 585 590
 Met Tyr Leu Thr Tyr Lys Leu Leu Ser Leu Arg Lys Gln Leu Ala Glu
 595 600 605
 Asp Phe Leu Lys Gly Glu Tyr Lys Gly Leu Asp Leu Glu Glu Gly Leu
 610 615 620
 Cys Gly Phe Ile Arg Phe Asn Lys Ile Leu Val Ile Ile Lys Thr Lys
 625 630 635 640
 Gly Ser Val Asn Tyr Lys Leu Lys Leu Glu Glu Gly Ala Ile Tyr Thr
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 <213> *Sulfolobus solfataricus*

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 gcagaggtaa acccatgaat gtcattttcg acgtattaaa cgagatccat gggttttttg 180
 gtgcattgtg ggcgggagca gctctactta actacttagt taagcctcaa gataagaggc 240
 aatttgagag aatagggaaa ttcttcatga taaactcagt cattacagta ataactggga 300
 taataatttt cgcctacatt tacctagccc cttatcaagg gaattttatt ctagtagcgg 360
 caattctacg ttcaagcctt gacattaggt taagggcctt actaaactta ataggaggag 420
 cgtttgggtt attggctttt ggggcaggga tagttataag caataggata aggcttatgg 480
 tacgtgttaa ggaagtgac gctacaatcc tagagttgag gaatagtatt gccaatattat 540

ctaaaaattag ttttaattcttc ttattacttt ccttagccat gatgatactt gctgggtcca	600
tagcacaagt tataagtttag agttgaaaga aaaattta atg acg ttt gct tat aaa	656
Met Thr Phe Ala Tyr Lys	
1 5	
ata gat gga aat gag gta atc ttt acc tta tgg gca cct tat caa aag	704
Ile Asp Gly Asn Glu Val Ile Phe Thr Leu Trp Ala Pro Tyr Gln Lys	
10 15 20	
agc gtt aaa cta aag gtt cta gag aag gga ctt tac gaa atg gaa aga	752
Ser Val Lys Leu Lys Val Leu Glu Lys Gly Leu Tyr Glu Met Glu Arg	
25 30 35	
gat gaa aaa ggt tac ttc acc att acc tta aac aac gta aag gtt aga	800
Asp Glu Lys Gly Tyr Phe Thr Ile Thr Leu Asn Asn Val Lys Val Arg	
40 45 50	
gat agg tat aaa tac gtt tta gat gat gct agt gaa ata cca gat cca	848
Asp Arg Tyr Lys Tyr Val Leu Asp Asp Ala Ser Glu Ile Pro Asp Pro	
55 60 65 70	
gca tcc aga tac caa cca gaa ggt gta cat ggg cct tca caa att ata	896
Ala Ser Arg Tyr Gln Pro Glu Gly Val His Gly Pro Ser Gln Ile Ile	
75 80 85	
caa gaa agt aaa gag ttc aac aac gag act ttt ctg aag aaa gag gac	944
Gln Glu Ser Lys Glu Phe Asn Asn Glu Thr Phe Leu Lys Lys Glu Asp	
90 95 100	
ttg ata att tat gaa ata cac gtg ggg act ttc act cca gag gga acg	992
Leu Ile Ile Tyr Glu Ile His Val Gly Thr Phe Thr Pro Glu Gly Thr	
105 110 115	
ttt gag gga gtg ata agg aaa ctt gac tac tta aag gat ttg gga att	1040
Phe Glu Gly Val Ile Arg Lys Leu Asp Tyr Leu Lys Asp Leu Gly Ile	
120 125 130	
acg gca ata gag ata atg cca ata gct caa ttt cct ggg aaa agg gat	1088
Thr Ala Ile Glu Ile Met Pro Ile Ala Gln Phe Pro Gly Lys Arg Asp	
135 140 145 150	
tgg ggt tat gat gga gtt tat tta tat gca gta cag aac tct tac gga	1136
Trp Gly Tyr Asp Gly Val Tyr Leu Tyr Ala Val Gln Asn Ser Tyr Gly	
155 160 165	
ggg cca gaa ggt ttt aga aag tta gtt gat gaa gcg cac aag aaa ggt	1184
Gly Pro Glu Gly Phe Arg Lys Leu Val Asp Glu Ala His Lys Lys Gly	
170 175 180	
tta gga gtt att tta gac gta gta tac aac cac gtt gga cca gag gga	1232
Leu Gly Val Ile Leu Asp Val Val Tyr Asn His Val Gly Pro Glu Gly	
185 190 195	
aac tat atg gtt aaa ttg ggg cca tat ttc tca cag aaa tac aaa acg	1280
Asn Tyr Met Val Lys Leu Gly Gly Pro Tyr Phe Ser Gln Lys Tyr Lys Thr	
200 205 210	

cca tgg gga tta acc ttt aac ttt gac gat gct gaa agc gat gag gtt Pro Trp Gly Leu Thr Phe Asn Phe Asp Asp Ala Glu Ser Asp Glu Val 215 220 225 230	1328
agg aag ttc atc tta gaa aac gtt gag tac tgg att aag gaa tat aac Arg Lys Phe Ile Leu Glu Asn Val Glu Tyr Trp Ile Lys Glu Tyr Asn 235 240 245	1376
gtt gat ggg ttt aga tta gat gcg gtt cat gca att att gac act tct Val Asp Gly Phe Arg Leu Asp Ala Val His Ala Ile Ile Asp Thr Ser 250 255 260	1424
cct aag cac atc ttg gag gaa ata gct gac gtt gtg cat aag tat aat Pro Lys His Ile Leu Glu Glu Ile Ala Asp Val Val His Lys Tyr Asn 265 270 275	1472
agg att gtc ata gcc gaa agt gat tta aac gat cct aga gtc gtt aat Arg Ile Val Ile Ala Glu Ser Asp Leu Asn Asp Pro Arg Val Val Asn 280 285 290	1520
ccc aag gaa aag tgt gga tat aat att gat gct caa tgg gtt gac gat Pro Lys Glu Lys Cys Gly Tyr Asn Ile Asp Ala Gln Trp Val Asp Asp 295 300 305 310	1568
ttc cat cat tct att cac gct tac tta act ggt gag agg caa ggc tat Phe His His Ser Ile His Ala Tyr Leu Thr Gly Glu Arg Gln Gly Tyr 315 320 325	1616
tat acg gat ttc ggt aac ctt gac gat ata gtt aaa tcg tat aag gac Tyr Thr Asp Phe Gly Asn Leu Asp Asp Ile Val Lys Ser Tyr Lys Asp 330 335 340	1664
gtt ttc gta tat gat ggt aag tac tcc aat ttt aga aga aaa act cac Val Phe Val Tyr Asp Gly Lys Tyr Ser Asn Phe Arg Arg Lys Thr His 345 350 355	1712
gga gaa cca gtt ggt gaa cta gac gga tgc aat ttc gta gtt tat ata Gly Glu Pro Val Gly Glu Leu Asp Gly Cys Asn Phe Val Val Tyr Ile 360 365 370	1760
caa aat cac gat caa gtc gga aat aga ggc aaa ggt gaa aga ata att Gln Asn His Asp Gln Val Gly Asn Arg Gly Lys Gly Glu Arg Ile Ile 375 380 385 390	1808
aaa tta gtc gat agg gaa agc tac aag atc gct gca gcc ctt tac ctt Lys Leu Val Asp Arg Glu Ser Tyr Lys Ile Ala Ala Ala Leu Tyr Leu 395 400 405	1856
ctt tcc ccc tat att cca atg att ttc atg gga gag gaa tac ggt gag Leu Ser Pro Tyr Ile Pro Met Ile Phe Met Gly Glu Glu Tyr Gly Glu 410 415 420	1904
gaa aat ccc ttt tat ttc ttt tct gat ttt tca gat tca aaa ctg ata Glu Asn Pro Phe Tyr Phe Phe Ser Asp Phe Ser Asp Ser Lys Leu Ile 425 430 435	1952

caa ggt gta agg gaa ggg aga aaa aag gaa aac ggg caa gat act gac 2000
 Gln Gly Val Arg Glu Gly Arg Lys Lys Glu Asn Gly Gln Asp Thr Asp
 440 445 450

cct caa gat gaa tca act ttt aac gct tcc aaa ctg agt tgg aag att 2048
 Pro Gln Asp Glu Ser Thr Phe Asn Ala Ser Lys Leu Ser Trp Lys Ile
 455 460 465 470

gac gag gaa atc ttt tca ttt tac aag att tta ata aaa atg aga aag 2096
 Asp Glu Glu Ile Phe Ser Phe Tyr Lys Ile Leu Ile Lys Met Arg Lys
 475 480 485

gag ttg agc ata gcg tgt gat agg aga gta aac gtc gtg aat ggc gaa 2144
 Glu Leu Ser Ile Ala Cys Asp Arg Arg Val Asn Val Val Asn Gly Glu
 490 495 500

aat tgg ttg atc atc aag gga aga gaa tac ttt tca ctc tac gtt ttc 2192
 Asn Trp Leu Ile Ile Lys Gly Arg Glu Tyr Phe Ser Leu Tyr Val Phe
 505 510 515

tct aaa tca tct att gaa gtt aag tac agt gga act tta ctt ttg tcc 2240
 Ser Lys Ser Ser Ile Glu Val Lys Tyr Ser Gly Thr Leu Leu Leu Ser
 520 525 530

tca aat aat tca ttc cct cag cat att gaa gaa ggt aaa tat gag ttt 2288
 Ser Asn Asn Ser Phe Pro Gln His Ile Glu Glu Gly Lys Tyr Glu Phe
 535 540 545 550

gat aag gga ttt gct tta tat aaa ctt taggacagga gagtttaaaa 2335
 Asp Lys Gly Phe Ala Leu Tyr Lys Leu
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atttctatga atgattatac tttagatgat gagtaaaagc aagatcgatg aggaagagaa 2395

aaggagaaga gaagaagtca aaaagttagt aatgctctta gcaatgttaa gataatgttt 2455

ttttaaactc aaataataat aaataccatc atgtcaatat tcttcagaac tagagataga 2515

cctttacgtc ccggagatcc gtatocatta ggttcaaatt ggatagaaga tgaggatggc 2575

gtaaattttt ccttggtctc agagaatgca gacaaagtgg agttgattct ttattcacia 2635

acaaatcaaa agtatccaaa ggagataata gaggttaaga atagaacggg ggatcc 2691

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 35 40 45
 Asn Val Lys Val Arg Asp Arg Tyr Lys Tyr Val Leu Asp Asp Ala Ser
 50 55 60
 Glu Ile Pro Asp Pro Ala Ser Arg Tyr Gln Pro Glu Gly Val His Gly
 65 70 75 80
 Pro Ser Gln Ile Ile Gln Glu Ser Lys Glu Phe Asn Asn Glu Thr Phe
 85 90 95
 Leu Lys Lys Glu Asp Leu Ile Ile Tyr Glu Ile His Val Gly Thr Phe
 100 105 110
 Thr Pro Glu Gly Thr Phe Glu Gly Val Ile Arg Lys Leu Asp Tyr Leu
 115 120 125
 Lys Asp Leu Gly Ile Thr Ala Ile Glu Ile Met Pro Ile Ala Gln Phe
 130 135 140
 Pro Gly Lys Arg Asp Trp Gly Tyr Asp Gly Val Tyr Leu Tyr Ala Val
 145 150 155 160
 Gln Asn Ser Tyr Gly Gly Pro Glu Gly Phe Arg Lys Leu Val Asp Glu
 165 170 175
 Ala His Lys Lys Gly Leu Gly Val Ile Leu Asp Val Val Tyr Asn His
 180 185 190
 Val Gly Pro Glu Gly Asn Tyr Met Val Lys Leu Gly Pro Tyr Phe Ser
 195 200 205
 Gln Lys Tyr Lys Thr Pro Trp Gly Leu Thr Phe Asn Phe Asp Asp Ala
 210 215 220
 Glu Ser Asp Glu Val Arg Lys Phe Ile Leu Glu Asn Val Glu Tyr Trp
 225 230 235 240
 Ile Lys Glu Tyr Asn Val Asp Gly Phe Arg Leu Asp Ala Val His Ala
 245 250 255
 Ile Ile Asp Thr Ser Pro Lys His Ile Leu Glu Glu Ile Ala Asp Val
 260 265 270
 Val His Lys Tyr Asn Arg Ile Val Ile Ala Glu Ser Asp Leu Asn Asp
 275 280 285
 Pro Arg Val Val Asn Pro Lys Glu Lys Cys Gly Tyr Asn Ile Asp Ala
 290 295 300
 Gln Trp Val Asp Asp Phe His His Ser Ile His Ala Tyr Leu Thr Gly
 305 310 315 320
 Glu Arg Gln Gly Tyr Tyr Thr Asp Phe Gly Asn Leu Asp Asp Ile Val
 325 330 335

Lys Ser Tyr Lys Asp Val Phe Val Tyr Asp Gly Lys Tyr Ser Asn Phe
 340 345 350
 Arg Arg Lys Thr His Gly Glu Pro Val Gly Glu Leu Asp Gly Cys Asn
 355 360 365
 Phe Val Val Tyr Ile Gln Asn His Asp Gln Val Gly Asn Arg Gly Lys
 370 375 380
 Gly Glu Arg Ile Ile Lys Leu Val Asp Arg Glu Ser Tyr Lys Ile Ala
 385 390 395 400
 Ala Ala Leu Tyr Leu Leu Ser Pro Tyr Ile Pro Met Ile Phe Met Gly
 405 410 415
 Glu Glu Tyr Gly Glu Glu Asn Pro Phe Tyr Phe Phe Ser Asp Phe Ser
 420 425 430
 Asp Ser Lys Leu Ile Gln Gly Val Arg Glu Gly Arg Lys Lys Glu Asn
 435 440 445
 Gly Gln Asp Thr Asp Pro Gln Asp Glu Ser Thr Phe Asn Ala Ser Lys
 450 455 460
 Leu Ser Trp Lys Ile Asp Glu Glu Ile Phe Ser Phe Tyr Lys Ile Leu
 465 470 475 480
 Ile Lys Met Arg Lys Glu Leu Ser Ile Ala Cys Asp Arg Arg Val Asn
 485 490 495
 Val Val Asn Gly Glu Asn Trp Leu Ile Ile Lys Gly Arg Glu Tyr Phe
 500 505 510
 Ser Leu Tyr Val Phe Ser Lys Ser Ser Ile Glu Val Lys Tyr Ser Gly
 515 520 525
 Thr Leu Leu Leu Ser Ser Asn Asn Ser Phe Pro Gln His Ile Glu Glu
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<210> 7

<211> 3600

<212> DNA

<213> *Sulfolobus acidocaldarius*

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<221> CDS

<222> (1176)..(2843)

<400> 7

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gcactaactc cgagctccgc gagtttagta gtcacgaatt tgcgtacata tttcggcgct 180
atccctttct catgcaataa attcttcgcy tagttgtacg ttatatcagt cttagctata 240
gacgaaatgt gaaagacata gaacactttc tttggccctc tagtccagtt gagcgtgtat 300
acgtagaagc cgtcctcttt caggttggtc ttctcgtcat actcattgag aacctttaca 360
gcctccctaa gccttatacc gctctcaagg aggagcttga agactagctc tacctcaata 420
cctctaacag cctccaacca cctccctatc tcgtcagctc ctggaacctt aagatcaaca 480
ccagactttt tcggttttcag cttttttccat gcctcaagat cccctttcca cttgtagaac 540
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tccttttccg tgagaccatt tttgcctcc ctagaagtaa gggagtttag ggcaaattccc 720
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caccaacgta agtctcttc gtcttaccac cttgactctt cttgataaag taaacataat 960
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ataactcaac aataataaga atttaatcag ttctgataag tatttttact cgaaaacatt 1140
taaatatatt aagacataat ttctatttta acagc atg ttt tcg ttc ggt gga 1193
Met Phe Ser Phe Gly Gly
1 5
aat att gaa aaa aat aaa ggt atc ttt aag tta tgg gca cct tat gtt 1241
Asn Ile Glu Lys Asn Lys Gly Ile Phe Lys Leu Trp Ala Pro Tyr Val
10 15 20
aat agt gtt aag ctg aag tta agc aaa aaa ctt att cca atg gaa aaa 1289
Asn Ser Val Lys Leu Lys Leu Ser Lys Lys Leu Ile Pro Met Glu Lys
25 30 35
aac gat gag gga ttt ttc gaa gta gaa ata gac gat atc gag gaa aat 1337
Asn Asp Glu Gly Phe Phe Glu Val Glu Ile Asp Asp Ile Glu Glu Asn
40 45 50
tta acc tat tct tat att ata gaa gat aag aga gag ata cct gat ccc 1385
Leu Thr Tyr Ser Tyr Ile Ile Glu Asp Lys Arg Glu Ile Pro Asp Pro
55 60 65 70
gca tca cga tat caa cct tta gga gtt cat gac aaa tca caa ctt ata 1433
Ala Ser Arg Tyr Gln Pro Leu Gly Val His Asp Lys Ser Gln Leu Ile
75 80 85

aga aca gat tat cag att ctt gac ctt gga aaa gta aaa ata gaa gat	1481
Arg Thr Asp Tyr Gln Ile Leu Asp Leu Gly Lys Val Lys Ile Glu Asp	
90 95 100	
cta ata ata tat gaa ctc cac gtt ggt act ttt tcc caa gaa gga aat	1529
Leu Ile Ile Tyr Glu Leu His Val Gly Thr Phe Ser Gln Glu Gly Asn	
105 110 115	
ttc aaa gga gta ata gaa aag tta gat tac ctc aag gat cta gga atc	1577
Phe Lys Gly Val Ile Glu Lys Leu Asp Tyr Leu Lys Asp Leu Gly Ile	
120 125 130	
aca gga att gaa ctg atg cct gtg gca caa ttt cca ggg aat aga gat	1625
Thr Gly Ile Glu Leu Met Pro Val Ala Gln Phe Pro Gly Asn Arg Asp	
135 140 145 150	
tgg gga tac gat ggt gtt ttt cta tac gca gtt caa aat act tat ggc	1673
Trp Gly Tyr Asp Gly Val Phe Leu Tyr Ala Val Gln Asn Thr Tyr Gly	
155 160 165	
gga cca tgg gaa ttg gct aag cta gta aac gag gca cat aaa agg gga	1721
Gly Pro Trp Glu Leu Ala Lys Leu Val Asn Glu Ala His Lys Arg Gly	
170 175 180	
ata gcc gta att ttg gat gtt gta tat aat cat ata ggt cct gag gga	1769
Ile Ala Val Ile Leu Asp Val Val Tyr Asn His Ile Gly Pro Glu Gly	
185 190 195	
aat tac ctt tta gga tta ggt cct tat ttt tca gac aga tat aaa act	1817
Asn Tyr Leu Leu Gly Leu Gly Pro Tyr Phe Ser Asp Arg Tyr Lys Thr	
200 205 210	
cca tgg gga tta aca ttt aat ttt gat gat agg gga tgt gat caa gtt	1865
Pro Trp Gly Leu Thr Phe Asn Phe Asp Asp Arg Gly Cys Asp Gln Val	
215 220 225 230	
aga aaa ttc att tta gaa aat gtc gag tat tgg ttt aag acc ttt aaa	1913
Arg Lys Phe Ile Leu Glu Asn Val Glu Tyr Trp Phe Lys Thr Phe Lys	
235 240 245	
atc gat ggt ctg aga ctg gat gca gtt cat gca att ttt gat aat tcg	1961
Ile Asp Gly Leu Arg Leu Asp Ala Val His Ala Ile Phe Asp Asn Ser	
250 255 260	
cct aag cat atc ctc caa gag ata gct gaa aaa gcc cat caa tta gga	2009
Pro Lys His Ile Leu Gln Glu Ile Ala Glu Lys Ala His Gln Leu Gly	
265 270 275	
aaa ttt gtt att gct gaa agt gat tta aat gat cca aaa ata gta aaa	2057
Lys Phe Val Ile Ala Glu Ser Asp Leu Asn Asp Pro Lys Ile Val Lys	
280 285 290	
gat gat tgt gga tat aaa ata gat gct caa tgg gtt gac gat ttc cac	2105
Asp Asp Cys Gly Tyr Lys Ile Asp Ala Gln Trp Val Asp Asp Phe His	
295 300 305 310	

cac gca gtt cat gca ttc ata aca aaa gaa aaa gat tat tat tac cag	2153
His Ala Val His Ala Phe Ile Thr Lys Glu Lys Asp Tyr Tyr Tyr Gln	
315 320 325	
gat ttt gga agg ata gaa gat ata gag aaa act ttt aaa gat gtt ttt	2201
Asp Phe Gly Arg Ile Glu Asp Ile Glu Lys Thr Phe Lys Asp Val Phe	
330 335 340	
gtt tat gat gga aag tat tct aga tac aga gga aga act cat ggt gct	2249
Val Tyr Asp Gly Lys Tyr Ser Arg Tyr Arg Gly Arg Thr His Gly Ala	
345 350 355	
cct gta ggt gat ctt cca cca cgt aaa ttt gta gtc ttc ata caa aat	2297
Pro Val Gly Asp Leu Pro Pro Arg Lys Phe Val Val Phe Ile Gln Asn	
360 365 370	
cac gat caa gta gga aat aga gga aat ggg gaa aga ctt tcc ata tta	2345
His Asp Gln Val Gly Asn Arg Gly Asn Gly Glu Arg Leu Ser Ile Leu	
375 380 385 390	
acc gat aaa acg aca tac ctt atg gca gcc aca cta tat ata ctc tca	2393
Thr Asp Lys Thr Thr Tyr Leu Met Ala Ala Thr Leu Tyr Ile Leu Ser	
395 400 405	
ccg tat ata ccg cta ata ttt atg ggc gag gaa tat tat gag acg aat	2441
Pro Tyr Ile Pro Leu Ile Phe Met Gly Glu Glu Tyr Tyr Glu Thr Asn	
410 415 420	
cct ttt ttc ttc ttc tct gat ttc tca gat ccc gta tta att aag ggt	2489
Pro Phe Phe Phe Phe Ser Asp Phe Ser Asp Pro Val Leu Ile Lys Gly	
425 430 435	
gtt aga gaa ggt aga cta aag gaa aat aat caa atg ata gat cca caa	2537
Val Arg Glu Gly Arg Leu Lys Glu Asn Asn Gln Met Ile Asp Pro Gln	
440 445 450	
tct gag gaa gcg ttc tta aag agt aaa ctt tca tgg aaa att gat gag	2585
Ser Glu Glu Ala Phe Leu Lys Ser Lys Leu Ser Trp Lys Ile Asp Glu	
455 460 465 470	
gaa gtt tta gat tat tat aaa caa ctg ata aat atc aga aag aga tat	2633
Glu Val Leu Asp Tyr Tyr Lys Gln Leu Ile Asn Ile Arg Lys Arg Tyr	
475 480 485	
aat aat tgt aaa agg gta aag gaa gtt agg aga gaa ggg aac tgt att	2681
Asn Asn Cys Lys Arg Val Lys Glu Val Arg Arg Glu Gly Asn Cys Ile	
490 495 500	
act ttg atc atg gaa aaa ata gga ata att gca tcg ttt gat gat att	2729
Thr Leu Ile Met Glu Lys Ile Gly Ile Ile Ala Ser Phe Asp Asp Ile	
505 510 515	
gta att aat tct aaa att aca ggt aat tta ctt ata ggc ata gga ttt	2777
Val Ile Asn Ser Lys Ile Thr Gly Asn Leu Leu Ile Gly Ile Gly Phe	
520 525 530	

ccg aaa aaa ttg aaa aaa gat gaa tta att aag gtt aac aga ggt gtt 2825
 Pro Lys Lys Leu Lys Lys Asp Glu Leu Ile Lys Val Asn Arg Gly Val
 535 540 545 550

ggg gta tat caa tta gaa tgaaagatcg accattaaag cctgggtgaac 2873
 Gly Val Tyr Gln Leu Glu
 555

cttatccttt aggggcaact tggatagagg aagaagatgg agttaatttt gtactattct 2933
 ctgagaacgc cacaaaagta gaactgttaa cgtactctca gactagacaa gatgagccaa 2993
 aggaaataat agaacttaga cagagaaccg gagatctctg gcatgttttt gtacctggtt 3053
 taagaccagg tcagttgtat gggtagagg tgtatgggcc atataaacca gaggaagggt 3113
 taaggtttaa tcctaataaa gtactgatag atccttatgc aaaagctata aacggattat 3173
 tactatggga tgattcggtc tttggatata aaattggaga tcagaaccag gatctcagtt 3233
 tcgatgagag aaaagacgat aaatttatac ctaaagggt cataataaat cttatttttg 3293
 attgggagga cgagcatttc ttctttagaa gaaagatacc ttttaaggat agtataattt 3353
 atgagacaca tataaaagga ataactaaat taaggcaaga tttaccggag aacgttagag 3413
 gcactttttt gggtttagca tcagatacta tgattgatta cctaaaagat ttaggaatta 3473
 caaccgttga gataatgcct attcagcaat ttgtagatga gagattcatt gtcgataaag 3533
 ggtaaagaa ctactggggt tacaatccga taaattattt ctctcctgaa tgtagatact 3593
 caagctc 3600

<210> 8

<211> 556

<212> PRT

<213> Sulfolobus acidocaldarius

<400> 8

Met Phe Ser Phe Gly Gly Asn Ile Glu Lys Asn Lys Gly Ile Phe Lys
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Leu Trp Ala Pro Tyr Val Asn Ser Val Lys Leu Lys Leu Ser Lys Lys
 20 25 30

Leu Ile Pro Met Glu Lys Asn Asp Glu Gly Phe Phe Glu Val Glu Ile
 35 40 45

Asp Asp Ile Glu Glu Asn Leu Thr Tyr Ser Tyr Ile Ile Glu Asp Lys
 50 55 60

Arg Glu Ile Pro Asp Pro Ala Ser Arg Tyr Gln Pro Leu Gly Val His
 65 70 75 80

Asp Lys Ser Gln Leu Ile Arg Thr Asp Tyr Gln Ile Leu Asp Leu Gly
 85 90 95

Lys Val Lys Ile Glu Asp Leu Ile Ile Tyr Glu Leu His Val Gly Thr
 100 105 110
 Phe Ser Gln Glu Gly Asn Phe Lys Gly Val Ile Glu Lys Leu Asp Tyr
 115 120 125
 Leu Lys Asp Leu Gly Ile Thr Gly Ile Glu Leu Met Pro Val Ala Gln
 130 135 140
 Phe Pro Gly Asn Arg Asp Trp Gly Tyr Asp Gly Val Phe Leu Tyr Ala
 145 150 155 160
 Val Gln Asn Thr Tyr Gly Gly Pro Trp Glu Leu Ala Lys Leu Val Asn
 165 170 175
 Glu Ala His Lys Arg Gly Ile Ala Val Ile Leu Asp Val Val Tyr Asn
 180 185 190
 His Ile Gly Pro Glu Gly Asn Tyr Leu Leu Gly Leu Gly Pro Tyr Phe
 195 200 205
 Ser Asp Arg Tyr Lys Thr Pro Trp Gly Leu Thr Phe Asn Phe Asp Asp
 210 215 220
 Arg Gly Cys Asp Gln Val Arg Lys Phe Ile Leu Glu Asn Val Glu Tyr
 225 230 235 240
 Trp Phe Lys Thr Phe Lys Ile Asp Gly Leu Arg Leu Asp Ala Val His
 245 250 255
 Ala Ile Phe Asp Asn Ser Pro Lys His Ile Leu Gln Glu Ile Ala Glu
 260 265 270
 Lys Ala His Gln Leu Gly Lys Phe Val Ile Ala Glu Ser Asp Leu Asn
 275 280 285
 Asp Pro Lys Ile Val Lys Asp Asp Cys Gly Tyr Lys Ile Asp Ala Gln
 290 295 300
 Trp Val Asp Asp Phe His His Ala Val His Ala Phe Ile Thr Lys Glu
 305 310 315 320
 Lys Asp Tyr Tyr Tyr Gln Asp Phe Gly Arg Ile Glu Asp Ile Glu Lys
 325 330 335
 Thr Phe Lys Asp Val Phe Val Tyr Asp Gly Lys Tyr Ser Arg Tyr Arg
 340 345 350
 Gly Arg Thr His Gly Ala Pro Val Gly Asp Leu Pro Pro Arg Lys Phe
 355 360 365
 Val Val Phe Ile Gln Asn His Asp Gln Val Gly Asn Arg Gly Asn Gly
 370 375 380
 Glu Arg Leu Ser Ile Leu Thr Asp Lys Thr Thr Tyr Leu Met Ala Ala
 385 390 395 400

Thr Leu Tyr Ile Leu Ser Pro Tyr Ile Pro Leu Ile Phe Met Gly Glu
 405 410 415
 Glu Tyr Tyr Glu Thr Asn Pro Phe Phe Phe Phe Ser Asp Phe Ser Asp
 420 425 430
 Pro Val Leu Ile Lys Gly Val Arg Glu Gly Arg Leu Lys Glu Asn Asn
 435 440 445
 Gln Met Ile Asp Pro Gln Ser Glu Glu Ala Phe Leu Lys Ser Lys Leu
 450 455 460
 Ser Trp Lys Ile Asp Glu Glu Val Leu Asp Tyr Tyr Lys Gln Leu Ile
 465 470 475 480
 Asn Ile Arg Lys Arg Tyr Asn Asn Cys Lys Arg Val Lys Glu Val Arg
 485 490 495
 Arg Glu Gly Asn Cys Ile Thr Leu Ile Met Glu Lys Ile Gly Ile Ile
 500 505 510
 Ala Ser Phe Asp Asp Ile Val Ile Asn Ser Lys Ile Thr Gly Asn Leu
 515 520 525
 Leu Ile Gly Ile Gly Phe Pro Lys Lys Leu Lys Lys Asp Glu Leu Ile
 530 535 540
 Lys Val Asn Arg Gly Val Gly Val Tyr Gln Leu Glu
 545 550 555

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 <212> PRT
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<400> 9
 Val Ile Arg Glu Ala Lys
 1 5

<210> 10
 <211> 6
 <212> PRT
 <213> Sulfolobus solfataricus

<400> 10
 Ile Ser Ile Arg Gln Lys
 1 5

<210> 11
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<400> 11
 Ile Ile Tyr Val Glu
 1 5

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<400> 12
 Met Leu Tyr Val Lys
 1 5

<210> 13
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 <212> PRT
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<400> 13
 Ile Leu Ser Ile Asn Glu Lys
 1 5

<210> 14
 <211> 7
 <212> PRT
 <213> Sulfolobus solfataricus

<400> 14
 Val Val Ile Leu Thr Glu Lys
 1 5

<210> 15
 <211> 10
 <212> PRT
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<400> 15
 Asn Leu Glu Leu Ser Asp Pro Arg Val Lys
 1 5 10

<210> 16
 <211> 12
 <212> PRT
 <213> Sulfolobus solfataricus

<400> 16
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 1 5 10

<210> 17
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<212> PRT
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<400> 17
 Val Ala Val Leu Phe Ser Pro Ile Val
 1 5

<210> 18
 <211> 11
 <212> PRT
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<400> 18
 Ile Asn Ile Asp Glu Leu Ile Ile Gln Ser Lys
 1 5 10

<210> 19
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 <212> PRT
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<400> 19
 Glu Leu Gly Val Ser His Leu Tyr Leu Ser Pro Ile
 1 5 10

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 Asp Tyr Phe Lys
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<400> 22
 Asp Gly Leu Tyr Asn Pro Lys
 1 5

<210> 23
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<212> PRT
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<400> 23
Asp Ile Asn Gly Ile Arg Glu Cys
1 5

<210> 24
<211> 7
<212> PRT
<213> Sulfolobus solfataricus

<400> 24
Asp Phe Glu Asn Phe Glu Lys
1 5

<210> 25
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<212> PRT
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<400> 25
Asp Leu Leu Arg Pro Asn Ile
1 5

<210> 26
<211> 5
<212> PRT
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<400> 26
Asp Ile Ile Glu Asn
1 5

<210> 27
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<400> 27
Asp Asn Ile Glu Tyr Arg Gly
1 5

<210> 28
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 28
ytcwckraaw acytcac

18

<210> 29
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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gataayatwg artayagrgg

20

<210> 30
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<400> 30
Arg Asn Pro Glu Ala Tyr Thr Lys
1 5

<210> 31
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<212> PRT
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<400> 31
Asp His Val Phe Gln Glu Ser His Ser
1 5

<210> 32
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<212> PRT
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<400> 32
Ile Thr Leu Asn Ala Thr Ser Thr
1 5

<210> 33
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<212> PRT
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<400> 33
Ile Ile Ile Val Glu Lys
1 5

<210> 34
<211> 11

<212> PRT

<213> Sulfolobus solfataricus

<400> 34

Leu Gln Gln Tyr Met Pro Ala Val Tyr Ala Lys
1 5 10

<210> 35

<211> 5

<212> PRT

<213> Sulfolobus solfataricus

<400> 35

Asn Met Leu Glu Ser
1 5

<210> 36

<211> 13

<212> PRT

<213> Sulfolobus solfataricus

<400> 36

Lys Ile Ser Pro Asp Gln Phe His Val Phe Asn Gln Lys
1 5 10

<210> 37

<211> 8

<212> PRT

<213> Sulfolobus solfataricus

<400> 37

Gln Leu Ala Glu Asp Phe Leu Lys
1 5

<210> 38

<211> 10

<212> PRT

<213> Sulfolobus solfataricus

<400> 38

Lys Ile Leu Gly Phe Gln Glu Glu Leu Lys
1 5 10

<210> 39

<211> 10

<212> PRT

<213> Sulfolobus solfataricus

<400> 39

Ile Ser Val Leu Ser Glu Phe Pro Glu Glu
1 5 10

<210> 40
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<400> 40
 Leu Lys Leu Glu Glu Gly Ala Ile Tyr
 1 5

<210> 41
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 <212> PRT
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<400> 41
 Glu Val Gln Ile Asn Glu Leu Pro
 1 5

<210> 42
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 <212> PRT
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<400> 42
 Asp His Ser Arg Ile
 1 5

<210> 43
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<400> 43
 Asp Leu Arg Tyr Tyr Lys
 1 5

<210> 44
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 <212> PRT
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<400> 44
 Asp Val Tyr Arg Thr Tyr Ala Asn Gln Ile Val Lys Glu Cys
 1 5 10

<210> 45
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<400> 45
 Thr Phe Ala Tyr Lys Ile Asp Gly Asn Glu
 1 5 10

<210> 46
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<400> 46
 Leu Gly Pro Tyr Phe Ser Gln
 1 5

<210> 47
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<400> 47
 Asp Val Phe Val Tyr Asp Gly
 1 5

<210> 48
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 <212> PRT
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<400> 48
 Tyr Asn Arg Ile Val Ile Ala Glu Ser Asp Leu Asn Asp Pro Arg Val
 1 5 10 15

Val Asn Pro

<210> 49
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 <212> PRT
 <213> Sulfolobus solfataricus

<400> 49
 Leu Asp Tyr Leu Lys
 1 5

<210> 50
 <211> 17
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<400> 50
 Lys Arg Glu Ile Pro Asp Pro Ala Ser Arg Tyr Gln Pro Leu Gly Val
 1 5 10 15

His

<210> 51
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 <212> PRT
 <213> Sulfolobus solfataricus

<400> 51
 Lys Asp Val Phe Val Tyr Asp Gly Lys
 1 5

<210> 52
 <211> 9
 <212> PRT
 <213> Sulfolobus solfataricus

<400> 52
 His Ile Leu Gln Glu Ile Ala Glu Lys
 1 5

<210> 53
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 <212> PRT
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<400> 53
 Lys Leu Trp Ala Pro Tyr Val Asn Ser Val
 1 5 10

<210> 54
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<400> 54
 Met Phe Ser Phe Gly Gly Asn
 1 5

<210> 55
 <211> 14
 <212> PRT
 <213> Sulfolobus solfataricus

<400> 55
 Asp Tyr Tyr Tyr Gln Asp Phe Gly Arg Ile Glu Asp Ile Glu
 1 5 10

<210> 56
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<400> 56
 Lys Ile Asp Ala Gln Trp Val
 1 5

<210> 57
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 57
 agcwagkagm taycarcc

18

<210> 58
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 58
 ytthccatcr tawacraawa catc

24

<210> 59
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<400> 59
 Asp Glu Phe Arg Glu Ser
 1 5

<210> 60
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<400> 60
 Asp Asn Ile Glu Tyr Arg Gly
 1 5

<210> 61
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<400> 61
 Pro Ala Ser Arg Tyr Gln Pro
 1 5

<210> 62
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 <212> PRT
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<400> 62
 Asp Val Phe Val Tyr Asp Gly Lys
 1 5

<210> 63
 <211> 559
 <212> PRT
 <213> Sulfolobus solfataricus

<400> 63
 Met Thr Phe Ala Tyr Lys Ile Asp Gly Asn Glu Val Ile Phe Thr Leu
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 Trp Ala Pro Tyr Gln Lys Ser Val Lys Leu Lys Val Leu Glu Lys Gly
 20 25 30
 Leu Tyr Glu Met Glu Arg Asp Glu Lys Gly Tyr Phe Thr Ile Thr Leu
 35 40 45
 Asn Asn Val Lys Val Arg Asp Arg Tyr Lys Tyr Val Leu Asp Asp Ala
 50 55 60
 Ser Glu Ile Pro Asp Pro Ala Ser Arg Tyr Gln Pro Glu Gly Val His
 65 70 75 80
 Gly Pro Ser Gln Ile Ile Gln Glu Ser Lys Glu Phe Asn Asn Glu Thr
 85 90 95
 Phe Leu Lys Lys Glu Asp Leu Ile Ile Tyr Glu Ile His Val Gly Thr
 100 105 110
 Phe Thr Pro Glu Gly Thr Phe Glu Gly Val Ile Arg Lys Leu Asp Tyr
 115 120 125
 Leu Lys Asp Leu Gly Ile Thr Ala Ile Glu Ile Met Pro Ile Ala Gln
 130 135 140
 Phe Pro Gly Lys Arg Asp Trp Gly Tyr Asp Gly Val Tyr Leu Tyr Ala
 145 150 155 160
 Val Gln Asn Ser Tyr Gly Gly Pro Glu Gly Phe Arg Lys Leu Val Asp
 165 170 175
 Glu Ala His Lys Lys Gly Leu Gly Val Ile Leu Asp Val Val Tyr Asn
 180 185 190
 His Val Gly Pro Glu Gly Asn Tyr Met Val Lys Leu Gly Pro Tyr Phe
 195 200 205
 Ser Gln Lys Tyr Lys Thr Pro Trp Gly Leu Thr Phe Asn Phe Asp Asp
 210 215 220

Ala Glu Ser Asp Glu Val Arg Lys Phe Ile Leu Glu Asn Val Glu Tyr
 225 230 235 240
 Trp Ile Lys Glu Tyr Asn Val Asp Gly Phe Arg Leu Asp Ala Val His
 245 250 255
 Ala Ile Ile Asp Thr Ser Pro Lys His Ile Leu Glu Glu Ile Ala Asp
 260 265 270
 Val Val His Lys Tyr Asn Arg Ile Val Ile Ala Glu Ser Asp Leu Asn
 275 280 285
 Asp Pro Arg Val Val Asn Pro Lys Glu Lys Cys Gly Tyr Asn Ile Asp
 290 295 300
 Ala Gln Trp Val Asp Asp Phe His His Ser Ile His Ala Tyr Leu Thr
 305 310 315 320
 Gly Glu Arg Gln Gly Tyr Tyr Thr Asp Phe Gly Asn Leu Asp Asp Ile
 325 330 335
 Val Lys Ser Tyr Lys Asp Val Phe Val Tyr Asp Gly Lys Tyr Ser Asn
 340 345 350
 Phe Arg Arg Lys Thr His Gly Glu Pro Val Gly Glu Leu Asp Gly Cys
 355 360 365
 Asn Phe Val Val Tyr Ile Gln Asn His Asp Gln Val Gly Asn Arg Gly
 370 375 380
 Lys Gly Glu Arg Ile Ile Lys Leu Val Asp Arg Glu Ser Tyr Lys Ile
 385 390 395 400
 Ala Ala Ala Leu Tyr Leu Leu Ser Pro Tyr Ile Pro Met Ile Phe Met
 405 410 415
 Gly Glu Glu Tyr Gly Glu Glu Asn Pro Phe Tyr Phe Phe Ser Asp Phe
 420 425 430
 Ser Asp Ser Lys Leu Ile Gln Gly Val Arg Glu Gly Arg Lys Lys Glu
 435 440 445
 Asn Gly Gln Asp Thr Asp Pro Gln Asp Glu Ser Thr Phe Asn Ala Ser
 450 455 460
 Lys Leu Ser Trp Lys Ile Asp Glu Glu Ile Phe Ser Phe Tyr Lys Ile
 465 470 475 480
 Leu Ile Lys Met Arg Lys Glu Leu Ser Ile Ala Cys Asp Arg Arg Val
 485 490 495
 Asn Val Val Asn Gly Glu Asn Trp Leu Ile Ile Lys Gly Arg Glu Tyr
 500 505 510
 Phe Ser Leu Tyr Val Phe Ser Lys Ser Ser Ile Glu Val Lys Tyr Ser
 515 520 525

Gly Thr Leu Leu Leu Ser Ser Asn Asn Ser Phe Pro Gln His Ile Glu
530 535 540

Glu Gly Lys Tyr Glu Phe Asp Lys Gly Phe Ala Leu Tyr Lys Leu
545 550 555